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Sharing knowledge.

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- However large a genetics department, it is very difficult to develop sufficient in-house case material to accurately interpret rare genetic variants, especially for complex cases, and to map and exclude benign genetic variants for all but the most common loci.
- While global databases exist, these are primarily for research purposes and often fail to meet clinics' standards of curation, phenotype annotation, population-specificity and clinical relevance. Nor do they permit the comparing of case history information and the sharing of clinical expertise, which are essential features of genetic medicine practice.
- Labs and clinics across the world are therefore banding together into consortia to share genetic data to commonly agreed formatting and annotation standards, tailored to a clinical context. Such data permit more accurate genetic mapping and interpretation and allow clinicians to compare notes on individual cases.

BENCH is the ideal genetic data management tool for such consortia:

- BENCH's standard patient information gathering and data transfer formats ensure data quality, integrity and compatibility across the consortium.
- This opens the door to joint charting of benign genetic variations in specific, locally relevant populations.
- BENCH's scoring and filtering algorithms allow much larger quantities of genotype- and phenotype-annotated case data to be mobilized in analyzing new cases.
- BENCH's data annotation systems permit comparisons of individual cases with true confidentiality.